

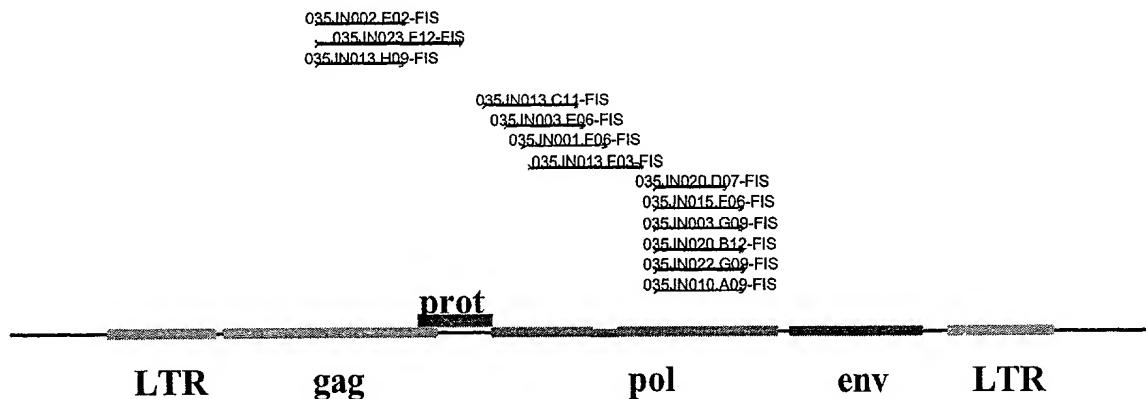
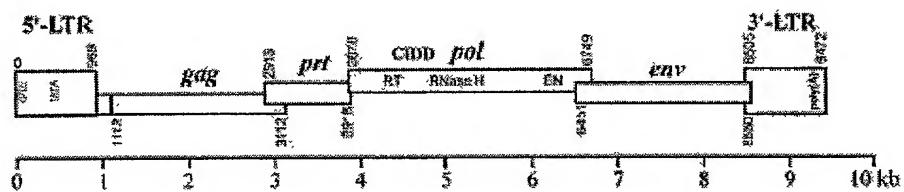
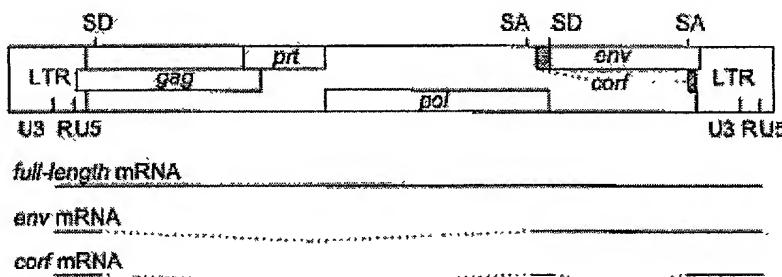
FIGURE 1**FIGURE 2****FIGURE 3**

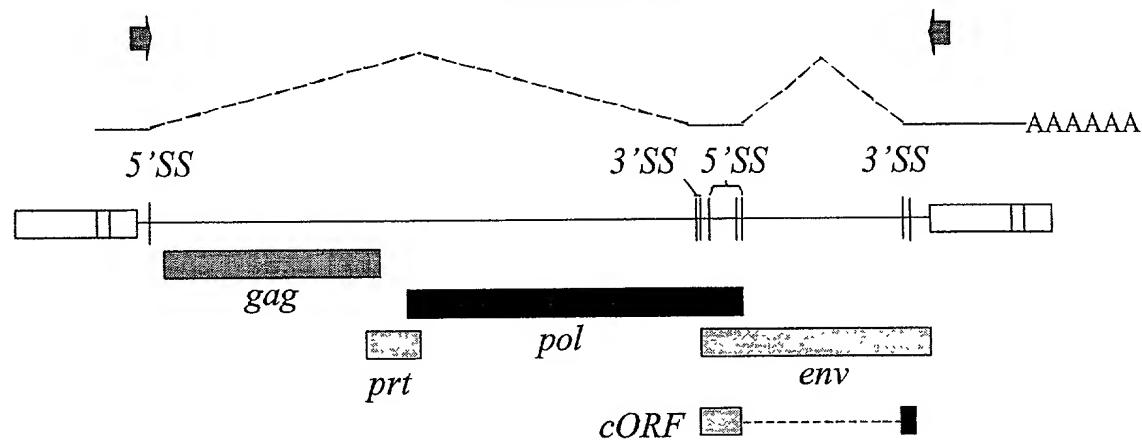
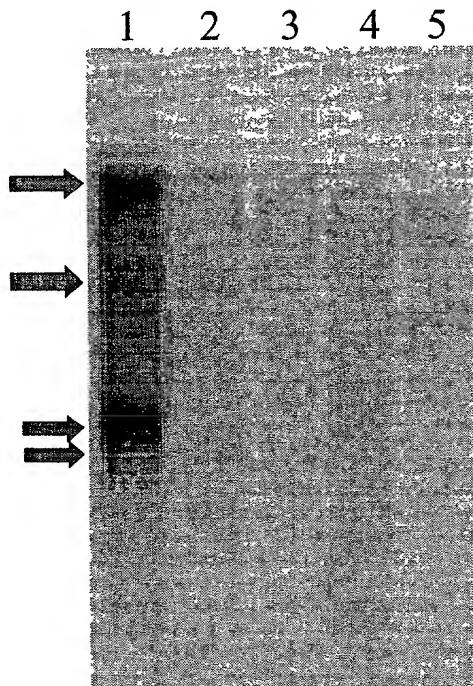
FIGURE 4**FIGURE 5**

FIGURE 6

1

ENV GENOMIC HERV MDA	(1)	-----	ACAGTTTAACTGTCGCA
ENV GENOMIC HERV-K TAN.	(1)	-----	ATGTTTCAAGCTTCGACA
ENV GENOMIC AC025420	(1)	-----	ACATTTTGACTTGACACA
ENV GENOMIC AP000776	(1)	-----	ACCTTTGAGCTTGACACA
ENV GENOMIC HERV-K8	(1)	-----	ACCTTTGAGCTTGACACA
ENV GENOMIC HERV-KI	(1)	-----	ACCTTTGAGCTTGACACA
ENV HERV-K AF023261	(1)	GGGGAGAGGTCTTGTGTTCACCAAGGAGAAAATCAGCTTCTGTTGGATAACCCACTAGACACATTGCGAGCTACA	-----
ENV GEN AL035086	(1)	-----	-----
ENV GENOMIC AL035587	(1)	-----	-----
ENV GENOMIC AC012068	(1)	-----	CTTACA
ENV GENOMIC AF277315	(1)	-----	CTTACA
ENV GENOMIC AF027650	(1)	GGGGAGAGGTCTTGTGTTCACCAAGGAGAAAATCAGCTTCTGTTGGATAACCCACTAGACACATTGCGAGCTACA	-----
ENV GENOMIC AC078899	(1)	-----	CTTACA
ENV GENOMIC HERV-KII	(1)	-----	CTTACA
ENV GENOMIC AC008813	(1)	-----	CTTACA
ENV GENOMIC AC012309	(1)	-----	CTTACA
ENV GENOMIC AL121932	(1)	-----	CTTACA
ENV GENOMIC AD000090	(1)	-----	CTTACA
ENV GEN AL160008	(1)	-----	CTTACA
ENV GENOMIC HEU32496	(1)	-----	CTTACA
ENV GENOMIC AC011467	(1)	-----	CTTACA
ENV GENOMIC AF235103	(1)	-----	CTTACA
ENV GENOMIC AC026786	(1)	-----	CTTACA
ENV GENOMIC AC034203	(1)	-----	CTTACA
ENV GENOMIC AC018809	(1)	-----	CTTACA
ENV GENOMIC HERV-K102 AF164610	(1)	-----	CTTACA
ENV GENOMIC FRAG. AF260253	(1)	-----	CTTACA
CONSENSUS	(1)	-----	ACATTGAAAGTTCTACA

80

ENV GENOMIC HERV MDA	(16)	-----	-----
ENV GENOMIC HERV-K TAN.	(18)	-----	GTTGAGATCTGGAGACACAGCTA
ENV GENOMIC AC025420	(18)	-----	ACGACCTGCGACAGGACATGCGACACAGCTA
ENV GENOMIC AP000776	(18)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC HERV-K8	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC HERV-KI	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV HERV-K AF023261	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GEN AL035086	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AL035587	(18)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC012068	(6)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AF277315	(15)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AF027650	(79)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC078899	(16)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC HERV-KII	(18)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC008813	(29)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC012309	(21)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AL121932	(18)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AD000090	(18)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GEN AL160008	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC HEU32496	(78)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC011467	(74)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AF235103	(72)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC026786	(58)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC034203	(58)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC AC018809	(16)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC HERV-K102 AF164610	(70)	-----	ATTCACCCCTTGACGGCTGACAGCTA
ENV GENOMIC FRAG. AF260253	(1)	-----	ATTCACCCCTTGACGGCTGACAGCTA
CONSENSUS	(81)	-----	ATGAACCCATC GAGATGCAAAGAA

160

ENV GENOMIC HERV MDA	(16)	-----	-----
ENV GENOMIC HERV-K TAN.	(18)	-----	-----
ENV GENOMIC AC025420	(18)	-----	-----
ENV GENOMIC AP000776	(18)	-----	-----
ENV GENOMIC HERV-K8	(1)	-----	-----
ENV GENOMIC HERV-KI	(1)	-----	-----
ENV HERV-K AF023261	(1)	-----	-----
ENV GEN AL035086	(1)	-----	-----
ENV GENOMIC AL035587	(18)	-----	-----
ENV GENOMIC AC012068	(6)	-----	-----
ENV GENOMIC AF277315	(15)	-----	-----
ENV GENOMIC AF027650	(79)	-----	-----
ENV GENOMIC AC078899	(16)	-----	-----
ENV GENOMIC HERV-KII	(18)	-----	-----
ENV GENOMIC AC008813	(29)	-----	-----
ENV GENOMIC AC012309	(21)	-----	-----
ENV GENOMIC AL121932	(18)	-----	-----
ENV GENOMIC AD000090	(18)	-----	-----
ENV GEN AL160008	(1)	-----	-----
ENV GENOMIC HEU32496	(78)	-----	-----
ENV GENOMIC AC011467	(74)	-----	-----
ENV GENOMIC AF235103	(72)	-----	-----
ENV GENOMIC AC026786	(58)	-----	-----
ENV GENOMIC AC034203	(58)	-----	-----
ENV GENOMIC AC018809	(16)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(70)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(81)	-----	AGC CCTCC CGGAGACGGAAACACCGCAATCGGCAC

81

ENV GENOMIC HERV MDA	(16)	-----	-----
ENV GENOMIC HERV-K TAN.	(18)	-----	-----
ENV GENOMIC AC025420	(18)	-----	-----
ENV GENOMIC AP000776	(18)	-----	-----
ENV GENOMIC HERV-K8	(1)	-----	-----
ENV GENOMIC HERV-KI	(1)	-----	-----
ENV HERV-K AF023261	(1)	-----	-----
ENV GEN AL035086	(1)	-----	-----
ENV GENOMIC AL035587	(18)	-----	-----
ENV GENOMIC AC012068	(6)	-----	-----
ENV GENOMIC AF277315	(15)	-----	-----
ENV GENOMIC AF027650	(79)	-----	-----
ENV GENOMIC AC078899	(16)	-----	-----
ENV GENOMIC HERV-KII	(18)	-----	-----
ENV GENOMIC AC008813	(29)	-----	-----
ENV GENOMIC AC012309	(21)	-----	-----
ENV GENOMIC AL121932	(18)	-----	-----
ENV GENOMIC AD000090	(18)	-----	-----
ENV GEN AL160008	(1)	-----	-----
ENV GENOMIC HEU32496	(78)	-----	-----
ENV GENOMIC AC011467	(74)	-----	-----
ENV GENOMIC AF235103	(72)	-----	-----
ENV GENOMIC AC026786	(58)	-----	-----
ENV GENOMIC AC034203	(58)	-----	-----
ENV GENOMIC AC018809	(16)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(70)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(81)	-----	ATGAACCCATC GAGATGCAAAGAA

161

ENV GENOMIC HERV MDA	(72)	-----	-----
ENV GENOMIC HERV-K TAN.	(83)	-----	-----
ENV GENOMIC AC025420	(83)	-----	-----
ENV GENOMIC AP000776	(83)	-----	-----
ENV GENOMIC HERV-K8	(15)	-----	-----
ENV GENOMIC HERV-KI	(83)	-----	-----
ENV HERV-K AF023261	(146)	-----	-----
ENV GEN AL035086	(1)	-----	-----
ENV GENOMIC AL035587	(83)	-----	-----
ENV GENOMIC AC012068	(71)	-----	-----
ENV GENOMIC AF277315	(80)	-----	-----
ENV GENOMIC AF027650	(144)	-----	-----
ENV GENOMIC AC078899	(81)	-----	-----
ENV GENOMIC HERV-KII	(72)	-----	-----
ENV GENOMIC AC008813	(104)	-----	-----
ENV GENOMIC AC012309	(86)	-----	-----
ENV GENOMIC AL121932	(83)	-----	-----
ENV GENOMIC AD000090	(88)	-----	-----
ENV GEN AL160008	(1)	-----	-----
ENV GENOMIC HEU32496	(143)	-----	-----
ENV GENOMIC AC011467	(128)	-----	-----
ENV GENOMIC AF235103	(142)	-----	-----
ENV GENOMIC AC026786	(58)	-----	-----
ENV GENOMIC AC034203	(123)	-----	-----
ENV GENOMIC AC018809	(70)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(124)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(161)	T GACTCACAGATGAA AAAATGGTGA TCAGAAGAACAGATGAAGTTGCCATCCACCAAGAA GC GA	-----

240

FIGURE 6 *contd.*

		321	
ENV GENOMIC HERV MDA	(139)	CTTCCGAAATACTGGGACATTAAAGAACCTTACACAGTTAGCTAAATAAAAGCTAATGAGTCACCA	
ENV GENOMIC HERV-K TAN.	(155)	GCCCCGAACTTGGGACACTAAAGGTTACCTACAAATA-TCTACAGCACACAAATCTACAGCAC	
ENV GENOMIC AC025420	(152)	CGCGCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AP000776	(87)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC HERV-K8	(155)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC HERV-KI	(218)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV HERV-K AF023261	(1)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GEN AL035086	(1)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AL035587	(155)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC012068	(143)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AF277315	(152)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AF027650	(216)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC078899	(153)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC HERV-KII	(72)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC008813	(176)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC012309	(154)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AL121932	(155)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AD000090	(168)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GEN AL160008	(34)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC HEU32496	(212)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC011467	(128)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AF235103	(204)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC026786	(91)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC034203	(195)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC AC018809	(70)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC HERV-K102 AF164610	(124)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
ENV GENOMIC FRAG. AF260253	(1)	CGCCCGACCTCGCCGCTTAACAGACCTGGCTTACCTAACTA-CGAGACATGACACA	
CONSENSUS	(241)	CGCCCGACCTGGGCACAA TAAAGAAGCTGACACAGTTAGCTA AAAA	CT GAGAACACAAAGGTGACACAA
		400	
ENV GENOMIC HERV MDA	(219)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HERV-K TAN.	(232)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC025420	(229)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AP000776	(232)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HERV-K8	(163)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HERV-KI	(232)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV HERV-K AF023261	(295)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GEN AL035086	(18)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AL035587	(232)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC012068	(220)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AF277315	(231)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AF027650	(294)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC078899	(231)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HERV-KII	(72)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC008813	(289)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC012309	(231)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AL121932	(232)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AD000090	(111)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GEN AL160008	(289)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HEU32496	(128)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC011467	(291)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AF235103	(169)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC026786	(272)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC034203	(70)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC AC018809	(124)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC HERV-K102 AF164610	(1)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
ENV GENOMIC FRAG. AF260253	(321)	TCCAGAGAAATACTGGGTTGGAGCCTGAGTATGATGAGCTGTTGATCTTGATGAGCACTG	
CONSENSUS			
		401	
ENV GENOMIC HERV MDA	(299)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HERV-K TAN.	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC025420	(309)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AP000776	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HERV-K8	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HERV-KI	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV HERV-K AF023261	(375)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GEN AL035086	(98)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AL035587	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC012068	(300)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AF277315	(309)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AF027650	(374)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC078899	(312)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HERV-KII	(72)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC008813	(332)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC012309	(311)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AL121932	(310)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AD000090	(325)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GEN AL160008	(191)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HEU32496	(369)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC011467	(128)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AF235103	(371)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC026786	(249)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC034203	(352)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC AC018809	(70)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC HERV-K102 AF164610	(124)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
ENV GENOMIC FRAG. AF260253	(1)	CGTAACTTAACTACTCGCTTAACGCCCTTGGGACCTTACACATGATATACTTAACTGAGCT	
CONSENSUS	(401)	GCTAA TATAC TACTGGGCTTATGCCCTTCCGGCCCTTATCGGGAGTCACATGGATGGATACTTATGAG	

FIGURE 6 contd...

ENV GENOMIC HERV MDA	(379)	181	AGGATTAATGAACTACGTCATGG ATACTTAAATGATAGCTATGG ATACTTAAATGATAGCTATGG WATGATAGCTATGG WATGATAGCTATGG	TGAGTGTCCAGATATGCTTCTCGCTGCGCTG TACCTGGCCCTTGATGATCTCGCTGCGCTG TACCTGGCCCTTGATGATCTCGCTGCGCTG TACCTGGCCCTTGATGATCTCGCTGCGCTG TACCTGGCCCTTGATGATCTCGCTGCGCTG	AGACATATGAG AGACATATGAG AGACATATGAG AGACATATGAG AGACATATGAG
ENV GENOMIC HERV-K TAN.	(392)				
ENV GENOMIC AC025420	(389)				
ENV GENOMIC AP000776	(392)				
ENV GENOMIC HERV-K8	(291)				
ENV GENOMIC HERV-KI	(392)				
ENV HERV-K AF023261	(455)				
ENV GEN AL035086	(178)				
ENV GENOMIC AL035587	(392)				
ENV GENOMIC AC012068	(380)				
ENV GENOMIC AF277315	(389)				
ENV GENOMIC AF027650	(454)				
ENV GENOMIC AC078899	(391)				
ENV GENOMIC HERV-KII	(100)				
ENV GENOMIC AC008813	(412)				
ENV GENOMIC AC012309	(391)				
ENV GENOMIC AL121932	(389)				
ENV GENOMIC AD000090	(405)				
ENV GEN AL160008	(271)				
ENV GENOMIC HEU32496	(441)				
ENV GENOMIC AC011467	(156)				
ENV GENOMIC AF235103	(451)				
ENV GENOMIC AC026786	(329)				
ENV GENOMIC AC034203	(432)				
ENV GENOMIC HERV-K102 AF164610	(98)				
ENV GENOMIC FRAG. AF260253	(1)				
CONSENSUS	(481)		ATATGTTAATATAGTGTATGGG	TACCTGGCCCCACAGATGATGTTGCGCTTGCCAAACCTGGAGAAGAAGGAATGATG	
		561			
ENV GENOMIC HERV MDA	(455)				
ENV GENOMIC HERV-K TAN.	(471)				
ENV GENOMIC AC025420	(468)				
ENV GENOMIC AP000776	(471)				
ENV GENOMIC HERV-K8	(291)				
ENV GENOMIC HERV-KI	(471)				
ENV HERV-K AF023261	(534)				
ENV GEN AL035086	(257)				
ENV GENOMIC AL035587	(471)				
ENV GENOMIC AC012068	(459)				
ENV GENOMIC AF277315	(468)				
ENV GENOMIC AF027650	(533)				
ENV GENOMIC AC078899	(470)				
ENV GENOMIC HERV-KII	(179)				
ENV GENOMIC AC008813	(491)				
ENV GENOMIC AC012309	(470)				
ENV GENOMIC AL121932	(468)				
ENV GENOMIC AD000090	(484)				
ENV GEN AL160008	(350)				
ENV GENOMIC HEU32496	(441)				
ENV GENOMIC AC011467	(235)				
ENV GENOMIC AF235103	(530)				
ENV GENOMIC AC026786	(405)				
ENV GENOMIC AC034203	(511)				
ENV GENOMIC AC018809	(178)				
ENV GENOMIC HERV-K102 AF164610	(231)				
ENV GENOMIC FRAG. AF260253	(1)				
CONSENSUS	(561)		ATATAATATTCCATTGGGTATC	TTATCCCTCTATTITGCCTTAGGGAGAGCACCAAGGATCTTAA	GCCTGCA TCCAAA
		641			
ENV GENOMIC HERV MDA	(534)				
ENV GENOMIC HERV-K TAN.	(550)				
ENV GENOMIC AC025420	(550)				
ENV GENOMIC AP000776	(550)				
ENV GENOMIC HERV-K8	(291)				
ENV GENOMIC HERV-KI	(550)				
ENV HERV-K AF023261	(613)				
ENV GEN AL035086	(336)				
ENV GENOMIC AL035587	(550)				
ENV GENOMIC AC012068	(538)				
ENV GENOMIC AF277315	(547)				
ENV GENOMIC AF027650	(612)				
ENV GENOMIC AC078899	(549)				
ENV GENOMIC HERV-KII	(258)				
ENV GENOMIC AC008813	(570)				
ENV GENOMIC AC012309	(549)				
ENV GENOMIC AL121932	(547)				
ENV GENOMIC AD000090	(563)				
ENV GEN AL160008	(429)				
ENV GENOMIC HEU32496	(441)				
ENV GENOMIC AC011467	(314)				
ENV GENOMIC AF235103	(609)				
ENV GENOMIC AC026786	(484)				
ENV GENOMIC AC034203	(590)				
ENV GENOMIC AC018809	(257)				
ENV GEN AL160008	(310)				
ENV GENOMIC HERV-K102 AF164610	(310)				
ENV GENOMIC FRAG. AF260253	(1)				
CONSENSUS	(641)		ATGGGTGGTAGAAGTACCTACTGTCACT	CCA CAGTAGATTCACTTACACATGGTAAG GG ATGTCATCAGGGCA	

FIGURE 6 *contd...*

721

ENV GENOMIC HERV MDA (609) -TAACTTAATTACGGGACCCCTCTTAAAGATCATTAATGAGGCTTGGCGAGGTGTCGAGAACAA
ENV GENOMIC HERV-K TAN. (630) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC025420 (627) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AP000776 (630) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC HERV-K8 (291) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC HERV-KI (630) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV HERV-K AF023261 (693) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GEN AL035086 (416) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AL035587 (630) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC012068 (618) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AF277315 (627) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AF027650 (692) CGGTTAAATTTTACAAACTTCTTCAAGATCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC078899 (629) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC HERV-KII (338) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC008813 (650) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC012309 (629) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AL121932 (627) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AD000090 (643) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GEN AL160008 (482) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC HEU32496 (441) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC011467 (394) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AF235103 (688) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC026786 (564) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC034203 (670) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC AC018809 (337) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC HERV-K102 AF164610 (390) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
ENV GENOMIC FRAG. AF260253 (1) TGCTTAAATTTTACAGGACCTTCTTCAAAACCTCTTAAATTTAGCTTACGAAACCTTCCCCAAAGGAAT
CONSENSUS (721) C GGTAAAT ATTACA GACTTTCTTATCAAAGATCATAAATTTAG CCTAAAGGGAAACCTTCCCCAAAGGAAT

801

ENV GENOMIC HERV MDA (685) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K TAN. (710) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC025420 (707) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AP000776 (710) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K8 (291) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-KI (710) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV HERV-K AF023261 (701) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GEN AL035086 (496) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AL035587 (710) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC012068 (698) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF277315 (707) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF027650 (700) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC078899 (709) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-KII (418) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC008813 (729) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC012309 (709) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AL121932 (707) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AD000090 (723) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GEN AL160008 (543) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HEU32496 (441) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC011467 (474) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF235103 (768) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC026786 (644) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC034203 (750) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC018809 (417) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K102 AF164610 (470) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC FRAG. AF260253 (1) TCCGAGAAGTCAAGGCCAGAGCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
CONSENSUS (801) TCCCRAAG ATCAAAA A CAGAAAGTTTAGTTGGGAGAATGTGTGGC AATAGTGC GTGATATTACAAACATG

881

ENV GENOMIC HERV MDA (764) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K TAN. (790) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC025420 (787) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AP000776 (790) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K8 (291) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-KI (790) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV HERV-K AF023261 (701) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GEN AL035086 (576) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AL035587 (790) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC012068 (778) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF277315 (787) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF027650 (700) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC078899 (789) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-KII (498) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC008813 (809) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC012309 (789) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AL121932 (787) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AD000090 (803) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GEN AL160008 (623) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HEU32496 (441) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC011467 (554) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AF235103 (848) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC026786 (724) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC034203 (830) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC AC018809 (497) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC HERV-K102 AF164610 (550) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
ENV GENOMIC FRAG. AF260253 (1) ATTTGAACTATTTATTTCTTCTTCTTGCTGTTGCTTGTGTTGTCGATTCATTC
CONSENSUS (881) AATTGGAACTATTATGAGTTGGGACCTCTGGGGTCAATTCTA CACA

960

FIGURE 6 *contd...*

FIGURE 6 CONTD...

		1201	1280
ENV GENOMIC HERV MDA	(967)	-----	-----
ENV GENOMIC HERV-K TAN.	(984)	-----	-----
ENV GENOMIC AC025420	(981)	-----	-----
ENV GENOMIC AP000776	(984)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(984)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(770)	-----	-----
ENV GENOMIC AL035587	(1017)	-----	-----
ENV GENOMIC AC012068	(981)	-----	-----
ENV GENOMIC AF277315	(990)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(1073)	CCACCCCGACTAACGCACATGCCACAGGGCTGTCACTCAGAAGTGTGAAACTCAAACCGATCCGCCCTACCCG	-----
ENV GENOMIC HERV-KII	(692)	-----	-----
ENV GENOMIC AC008813	(1003)	-----	-----
ENV GENOMIC AC012309	(983)	-----	-----
ENV GENOMIC AL121932	(981)	-----	-----
ENV GENOMIC AD000090	(997)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(683)	-----	-----
ENV GENOMIC AF235103	(1051)	-----	-----
ENV GENOMIC AC026786	(927)	-----	-----
ENV GENOMIC AC034203	(1033)	-----	-----
ENV GENOMIC AC018809	(691)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(744)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(1201)	-----	-----
		1281	1360
ENV GENOMIC HERV MDA	(967)	-----	-----
ENV GENOMIC HERV-K TAN.	(984)	-----	-----
ENV GENOMIC AC025420	(981)	-----	-----
ENV GENOMIC AP000776	(984)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(984)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(770)	-----	-----
ENV GENOMIC AL035587	(1017)	-----	-----
ENV GENOMIC AC012068	(981)	-----	-----
ENV GENOMIC AF277315	(990)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(1153)	ACCACCTCACCCAGCATCCATAAAAGCGGGCTGCACCTTTGCACAGCGTGACTTCCCTGGCGGACCAAGTGAACCTC	-----
ENV GENOMIC HERV-KII	(692)	-----	-----
ENV GENOMIC AC008813	(1003)	-----	-----
ENV GENOMIC AC012309	(983)	-----	-----
ENV GENOMIC AL121932	(981)	-----	-----
ENV GENOMIC AD000090	(997)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(683)	-----	-----
ENV GENOMIC AF235103	(1051)	-----	-----
ENV GENOMIC AC026786	(927)	-----	-----
ENV GENOMIC AC034203	(1033)	-----	-----
ENV GENOMIC AC018809	(691)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(744)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(1281)	-----	-----
		1361	1440
ENV GENOMIC HERV MDA	(967)	-----	-----
ENV GENOMIC HERV-K TAN.	(984)	-----	-----
ENV GENOMIC AC025420	(981)	-----	-----
ENV GENOMIC AP000776	(984)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(984)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(770)	-----	-----
ENV GENOMIC AL035587	(1017)	-----	-----
ENV GENOMIC AC012068	(981)	-----	-----
ENV GENOMIC AP277315	(990)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(1233)	ACCGGAGAGCTCAATAAAGAAGATTTTGCCCTTTGCTTGGCTCTGGCCATTATGATCCACGGTGCCCTTCCATTG	-----
ENV GENOMIC HERV-KII	(692)	-----	-----
ENV GENOMIC AC008813	(1003)	-----	-----
ENV GENOMIC AC012309	(983)	-----	-----
ENV GENOMIC AL121932	(981)	-----	-----
ENV GENOMIC AD000090	(997)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(683)	-----	-----
ENV GENOMIC AF235103	(1051)	-----	-----
ENV GENOMIC AC026786	(927)	-----	-----
ENV GENOMIC AC034203	(1033)	-----	-----
ENV GENOMIC AC018809	(691)	-----	-----
ENV GENOMIC HERV-K102 AF164610	(744)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(1361)	-----	-----

FIGURE 6 *contd...*

FIGURE 6 contd...

1681

ENV GENOMIC HERV MDA	(1190)	CCAGCTTCCCAGACTATA	ATCTGTCGAAATTGCAAGTGTTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HERV-K TAN.	(1209)	CCAGACCTCCGAGCTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC025420	(1206)	CCAGCTTCCCAGACTATA	CCCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AP000776	(1209)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HERV-K8	(291)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HERV-K1	(1209)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV HERV-K AF023261	(701)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GEN GEN AL035086	(995)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AL035587	(1242)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC012068	(1202)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AF277315	(1215)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AF027650	(700)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC078899	(1549)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HERV-KII	(913)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC008813	(1228)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC012309	(1208)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AL121932	(1207)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AD000090	(1220)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GEN AL160008	(647)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HEU32496	(441)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC011467	(883)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AP235103	(1276)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC026786	(1152)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC034203	(1258)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC AC018809	(916)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC HERV-K102 AF164610	(969)	CCAGCTTCCCAGACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
ENV GENOMIC FRAG. AF260253	(1)		ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT
CONSENSUS	(1681)	CCAGA TCCCCAACTATA	ACCTCTGCAAAATTGTAGATTCCTACTTCATGGACCTTAATGGCAGCACCGT

1760

1761

ENV GENOMIC HERV MDA	(1268)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	1840
ENV GENOMIC HERV-K TAN.	(1287)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AC025420	(1284)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AP000776	(1287)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC HERV-K8	(291)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC HERV-K1	(1287)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV HERV-K AF023261	(701)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GEN AL035086	(1073)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AL035587	(1320)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AC012068	(1280)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AF277315	(1293)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AF027650	(700)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AC078899	(1627)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC HERV-KII	(991)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AC008813	(1238)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AC012309	(1288)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AL121932	(1285)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GENOMIC AD000090	(1298)	ATTCCTACAGAACACCCACAGGCGCTTTCGCGCTCTTCGCGATGACCGCG	
ENV GEN AL160008	(647)		
ENV GENOMIC HEU32496	(441)		
ENV GENOMIC AC011467	(961)		
ENV GENOMIC AP235103	(1354)		
ENV GENOMIC AC026786	(1230)		
ENV GENOMIC AC034203	(1336)		
ENV GENOMIC AC018809	(992)		
ENV GENOMIC HERV-K102 AF164610	(1047)		
ENV GENOMIC FRAG. AF260253	(1)		
CONSENSUS	(1761)	ATTCCTG GTGAGAGCAAGAGA GG GGTGGATCCCTGTCATGGACCGACCGTGGGGTC	CCATCC TCCA

1840

1841

ENV GENOMIC HERV MDA	(1348)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	1820
ENV GENOMIC HERV-K TAN.	(1367)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AC025420	(1364)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AP000776	(1367)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC HERV-K8	(291)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC HERV-K1	(1367)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV HERV-K AF023261	(701)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GEN AL035086	(1153)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AL035587	(1399)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AC012068	(1360)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AF277315	(1373)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AF027650	(700)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AC078899	(1707)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC HERV-KII	(1071)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AC008813	(1238)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AC012309	(1368)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AL121932	(1365)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GENOMIC AD000090	(1378)	TATTTTATGGAACTTAAACAGAACATTAACTACAGATCAATTACTTCATGGCG	
ENV GEN AL160008	(647)		
ENV GENOMIC HEU32496	(441)		
ENV GENOMIC AC011467	(1041)		
ENV GENOMIC AP235103	(1434)		
ENV GENOMIC AC026786	(1310)		
ENV GENOMIC AC034203	(1403)		
ENV GENOMIC AC018809	(1072)		
ENV GENOMIC HERV-K102 AF164610	(1127)		
ENV GENOMIC FRAG. AF260253	(1)		
CONSENSUS	(1841)	TATTTT AC GAGTATTAAAAGG TT TAA TAGATCCAAAAGAGTCATTTTACTTTAATTGCACTGATTATGGG	

FIGURE 6 contd...

2000

ENV GENOMIC HERV MDA	(1428)	TCCTTGCACTGCAAGTGTGCTGGCTGCTGGATTGCTTTAACAGCTGCTTTCACATCCTGAAACCTTAACGAT
ENV GENOMIC HERV-K TAN.	(1447)	TAATTCGGCAAGCGCAAGGCTGCTTACGTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC025420	(1444)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AP000776	(1447)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC HERV-K8	(291)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC HERV-KI	(1447)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV HERV-K AF023261	(701)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GEN AL035086	(1233)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AL035587	(1475)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC012068	(1440)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AF277315	(1453)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AF027650	(700)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC078899	(1786)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC HERV-KII	(1151)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC008813	(1238)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC012309	(1448)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AL121932	(1444)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AD000090	(1458)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GEN AL160008	(647)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC HEU32496	(441)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC011467	(1121)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AF235103	(1514)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC026786	(1390)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC034203	(1403)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC AC018809	(1151)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC HERV-K102 AF164610	(1207)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
ENV GENOMIC FRAG. AF260253	(1)	TAATTCGGCAAGCGCAAGGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGAT
CONSENSUS	(1921)	T ATTGCACTCACAGCTAC GCTGC G GC GGA TTGC TT CACTC TCTGTCA C G A A T TGT AT AT

2001

ENV GENOMIC HERV MDA	(1508)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HERV-K TAN.	(1527)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC025420	(1524)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AP000776	(1527)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HERV-K8	(291)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HERV-KI	(1527)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV HERV-K AF023261	(701)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GEN AL035086	(1313)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AL035587	(1555)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC012068	(1520)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AF277315	(1533)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AF027650	(700)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC078899	(1788)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HERV-KII	(1231)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC008813	(1238)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC012309	(1528)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AL121932	(1524)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AD000090	(1538)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GEN AL160008	(647)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HEU32496	(441)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC011467	(1201)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AF235103	(1594)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC026786	(1470)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC034203	(1403)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC AC018809	(1231)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC HERV-K102 AF164610	(1287)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
ENV GENOMIC FRAG. AF260253	(1)	TCGCCAAAGAT - TTCTCTAATTTGCGGATTTTCGCTCAA - AAAATACTAAAATTCGCAACCATTAAATGATTT
CONSENSUS	(2001)	TGGCAAAA AA TTC CAA ATTGTGAAATTC CA A C AT GATCAAAATTGGCAAAATCAAATTAATGATCTT

2081

ENV GENOMIC HERV MDA	(1586)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HERV-K TAN.	(1605)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC025420	(1602)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AP000776	(1605)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HERV-K8	(291)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HERV-KI	(1605)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV HERV-K AF023261	(701)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GEN AL035086	(1392)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AL035587	(1633)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC012068	(1598)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AF277315	(1611)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AF027650	(700)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC078899	(1864)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HERV-KII	(1309)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC008813	(1238)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC012309	(1606)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AL121932	(1538)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AD000090	(1616)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GEN AL160008	(647)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HEU32496	(441)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC011467	(1279)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AF235103	(1672)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC026786	(1548)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC034203	(1403)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC AC018809	(1309)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC HERV-K102 AF164610	(1365)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
ENV GENOMIC FRAG. AF260253	(1)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG
CONSENSUS	(2081)	AGACAAACTGCAATTGGATGAG - AGCGCATGAGCTGGATGAGTTCTTTCAGCTGGAGTTGAGCTGAGCTGAGCTGAG

FIGURE 6 *contd...*

FIGURE 6 *contd...*

FIGURE 6 contd...

	2641	2707
ENV GENOMIC HERV MDA	(2136)	
ENV GENOMIC HERV-K TAN.	(2146)	
ENV GENOMIC AC025420	(2143)	
ENV GENOMIC AP000776	(2146)	
ENV GENOMIC HERV-K8	(291)	
ENV GENOMIC HERV-KI	(2141)	
ENV HERV-K AF023261	(701)	
ENV GEN AL035086	(1931)	
ENV GENOMIC AL035587	(2146)	
ENV GENOMIC AC012068	(2138)	
ENV GENOMIC AF277315	(2152)	
ENV GENOMIC AF027650	(700)	
ENV GENOMIC AC078899	(2405)	
ENV GENOMIC HERV-KII	(1850)	
ENV GENOMIC AC008813	(1238)	
ENV GENOMIC AC012309	(2133)	
ENV GENOMIC AL121932	(1538)	
ENV GENOMIC AD000090	(2157)	
ENV GEN AL160008	(647)	
ENV GENOMIC HEU32496	(441)	
ENV GENOMIC AC011467	(1699)	
ENV GENOMIC AF235103	(2212)	
ENV GENOMIC AC026786	(2086)	
ENV GENOMIC AC034203	(1403)	
ENV GENOMIC AC018809	(1846)	
ENV GENOMIC HERV-K102 AF164610	(1906)	
ENV GENOMIC FRAG. AF260253	(385)	
CONSENSUS	(2641) TG	TGTAC

FIGURE 7

	1	60
GI_4185938_EMB_CAA76878.1_	(1) -----MGQTKSKIKSKYASYLSPFIKILLKRGGVKVSTKNLKLFOIIEQFCPWFPPEQGTL	
GI_4185942_EMB_CAA76881.1_	(1) -----MGQTKSKIKSKYASYLSPFIKILLKRGGVKVSTKNLKLFOIIEQFCPWFPPEQGTL	
GI_4185946_EMB_CAA76884.1_	(1) -----MGQTKSKIKSKYASYLSPFIKILLKRGGVKVSTKNLKLFOIIEQFCPWFPPEQGTL	
GI_5931704_EMB_CAB56602.1_	(1) -----MGQTKTFSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
GAG OF AB047240	(1) -----MGQTKSFTSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
TRANSLATION OF ORF99	(1) -----MGQTKSFTSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
TRANSLATION OF G226TOP-LINK	(1) -----MGQTKSFTSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
TRANSLATION OF G591TOP-LINK	(1) -----MGQTKSFTSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
TRANSLATION OF LNCAP-GAG	(1) -----MGQTKSFTSKTSKYASYLSPFIKILLKRGGVRVSTKNLKLFOIIEQFCPWFPPEQGTL	
GAG106-135	(1) -----	
GAG186-215	(1) -----	
GAG46-75	(1) -----	
PDG-G1	(1) -----	
PGD-G2	(1) -----	
PGD-G3	(1) -----	
CONSENSUS	(1) -----CPWFPEQG L	

	61	120
GI_4185938_EMB_CAA76878.1_	(56) DLKDWRIGKELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
GI_4185942_EMB_CAA76881.1_	(56) DLKDWRIGKELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
GI_4185946_EMB_CAA76884.1_	(56) DLKDWRIGKELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
GI_5931704_EMB_CAB56602.1_	(54) DLEDWKRIGKELKQAGRKGNIIPLTWWNDWPIKAALEPFQTEEDSVSVSDAPGSC IDC	
GAG OF AB047240	(56) DLKDWRIGEELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
TRANSLATION OF ORF99	(61) DLKDWRIGEELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
TRANSLATION OF G226TOP-LINK	(1) -----	
TRANSLATION OF G591TOP-LINK	(1) -----	
TRANSLATION OF LNCAP-GAG	(56) DLKDWRIGEELKQAGRKGNIIPLTWWNDWAIKAALEPFQTEEDSVSVSDAPGSC IDC	
GAG106-135	(1) -----	
GAG186-215	(1) -----	
GAG46-75	(11) DLKDWRIGKELKQAGRKG-----	
PDG-G1	(1) ---DWKRIGKELKQAGRKG-----	
PGD-G2	(1) -----	
PGD-G3	(1) -----	
CONSENSUS	(61) DL DWKRIG ELKQAGRKG----- DAPGSCI IDC	

FIGURE 7 CONTD...

GI_4185938_EMB_CAA76878.1_	(116) NENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS	121	180
GI_4185942_EMB_CAA76881.1_	(116) NENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS		
GI_4185946_EMB_CAA76884.1_	(116) NENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS		
GI_5931704_EMB_CAB56602.1_	(113) NEKTRKKSQKETETLHCEYVAEPLMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPLE		
GAG OF AB047240	(116) NEKTRGRKSQKETETLHCEYVTEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS		
TRANSLATION OF ORF99	(121) NEKTRGRKSQKETETLHCEYVTEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS		
TRANSLATION OF G226TOP-LINK	(1)		
TRANSLATION OF G591TOP-LINK	(1)		
TRANSLATION OF LNCAP-GAG	(116) NEKTRGRKSQKETETLHCEYVTEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGP ELVGPS		
GAG106-135	(11) NENTRKKSQKETEGLHCEYV-----		
GAG186-215	(1)		
GAG46-75	(31) -----		
PDG-G1	(17) -----		
PGD-G2	(1) -----		
PGD-G3	(1) -----		
CONSENSUS	(121) NE T KKSQKETE LHCEYV		
GI_4185938_EMB_CAA76878.1_	(176) SKPRGTSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYRPP PESQYGYPGMPP	181	240
GI_4185942_EMB_CAA76881.1_	(176) SKPRGTSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYRPP PESQYGYPGMPP		
GI_4185946_EMB_CAA76884.1_	(176) SKPRGTSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYRPP PESQYGYPGMPP		
GI_5931704_EMB_CAB56602.1_	(173) SKPRGSPSLSAGQVTVTLQPKQAVKENKTQLPVAYQYWPPAELQYRPP PESQYGYLGMP		
GAG OF AB047240	(176) SKPRGSPSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYLP PPPESQYGYPGMPP		
TRANSLATION OF ORF99	(181) SKPRGSPSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYLP PPPESQYGYPGMPP		
TRANSLATION OF G226TOP-LINK	(1)		
TRANSLATION OF G591TOP-LINK	(1)		
TRANSLATION OF LNCAP-GAG	(176) SKPRGSPSPLPAGQVPVTILOPQPKQVKENKTQPPVAYQYWPPAELQYLP PPPESQYGYPGMPP		
GAG106-135	(31) -----		
GAG186-215	(1) -----AGQVPVTILOPOKOVKENKTQPPVAYQYWPP-----		
GAG46-75	(31) -----		
PDG-G1	(17) -----		
PGD-G2	(1) -----		
PGD-G3	(1) -----		
CONSENSUS	(181) AGQV VTLQPQ QVKENKTQ PVAYQYWPP	SQGYGY GMPP	
GI_4185938_EMB_CAA76878.1_	(236) APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPVTLEPM PPGEGA	241	300
GI_4185942_EMB_CAA76881.1_	(236) APQGRAPYPQPPTTRLNPTAPPSRRGSELHEIIDKSRKEGDTEAWQFPV MLEPMPPGEGA		
GI_4185946_EMB_CAA76884.1_	(236) APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPV MLEPMPPGEGA		
GI_5931704_EMB_CAB56602.1_	(233) APQDREPYQPQPPTRRQCYGTT		
GAG OF AB047240	(236) ALQGRAPYPQPPTVRLNPTASRGQGGTLHAVIDEARKQGDLEAWRFLV ILQLVQAGEET		
TRANSLATION OF ORF99	(241) ALQGRAPYPQPPTVRLNPTASRGQGGTLHAVIDEARKQGDLEAWRFLV ILQLVQAGEET		
TRANSLATION OF G226TOP-LINK	(11) APQGRAPYPQPPTTRLNPTA-----		
TRANSLATION OF G591TOP-LINK	(1)		
TRANSLATION OF LNCAP-GAG	(236) ALQGRAPYPQPPTVRLNPTASRGQGGTLHAVIDEARKQGDLEAWRFLV ILQLVQAGEET		
GAG106-135	(31) -----		
GAG186-215	(31) -----		
GAG46-75	(31) -----		
PDG-G1	(17) -----		
PGD-G2	(1) -----SKLHEIIDKSRKEGD-----		
PGD-G3	(1) -----		
CONSENSUS	(241) A Q R PYPQPPT R		
GI_4185938_EMB_CAA76878.1_	(296) QEGEPPPTVEARYKSFISIKKLKDMKEGVKQYGPNSPYMRTLLDSIAH GHRLIPYDWEILAK	301	360
GI_4185942_EMB_CAA76881.1_	(296) QEGEPPPTVEARYKSFISIKMLKDMKEGVKQYGPNSPYMRTLLDSIAH GHRLIPYDWEILAK		
GI_4185946_EMB_CAA76884.1_	(296) QEGEPPPTVEARYKSFISIKKLKDMKEGVKQYGPNSPYMRTLLDSIAH GHRLIPYDWEILAK		
GI_5931704_EMB_CAB56602.1_	(254) -----		
GAG OF AB047240	(296) QVGAPARAETRCEPFTMKMLDIKEGVKQYGSNSPYIRTLLDSIAHGNR LTPDWEISLAK		
TRANSLATION OF ORF99	(301) QVGAPARAETRCEPFTMKMLDIKEGVKQYGSNSPYIRTLLDSIAHGNR LTPDWEISLAK		
TRANSLATION OF G226TOP-LINK	(31) -----		
TRANSLATION OF G591TOP-LINK	(1)		
TRANSLATION OF LNCAP-GAG	(296) QVGAPARAETRCEPFTMKMLDIKEGVKQYGSNSPYIRTLLDSIAHGNR LTPDWEISLAK		
GAG106-135	(31) -----		
GAG186-215	(31) -----		
GAG46-75	(31) -----		
PDG-G1	(17) -----		
PGD-G2	(17) -----		
PGD-G3	(1) -----		
CONSENSUS	(301)		

FIGURE 7 CONTD...

GI_4185938_EMB_CAA76878.1_	361	420
GI_4185942_EMB_CAA76881.1_	(356)	SSLSPSQFLQFKTWWIDGVQEQRNRRAANPPVNIDADQLLGIGQNWTISQQALMQNEA
GI_4185946_EMB_CAA76884.1_	(356)	SSLSPSQFLQFKTWWIDGVQEQRNRRAANPPVNIDADQLLGIGQNWTISQQALMQNEA
GI_5931704_EMB_CAB56602.1_	(254)	-----
GAG OF AB047240	(356)	SSLSSSQYLQFKTWWIDGVQEQRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
TRANSLATION OF ORF99	(361)	SSLSSSQYLQFKTWWIDGVQEQRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
TRANSLATION OF G226TOP-LINK	(31)	-----
TRANSLATION OF G591TOP-LINK	(1)	-----
TRANSLATION OF LNCAP-GAG	(356)	SSLSSSQYLQFKTWWIDGVQEQRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
GAG106-135	(31)	-----
GAG186-215	(31)	-----
GAG46-75	(31)	-----
PDG-G1	(17)	-----
PGD-G2	(17)	-----
PGD-G3	(1)	-----
CONSENSUS	(361)	-----
GI_4185938_EMB_CAA76878.1_	421	480
GI_4185942_EMB_CAA76881.1_	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
GI_4185946_EMB_CAA76884.1_	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
GI_5931704_EMB_CAB56602.1_	(254)	-----
GAG OF AB047240	(416)	IEQVRAICLRAWGKIQDPGTAFF-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
TRANSLATION OF ORF99	(421)	IEQVRAICLRAWGKIQDPGTAFF-PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
TRANSLATION OF G226TOP-LINK	(31)	-----
TRANSLATION OF G591TOP-LINK	(1)	-----
TRANSLATION OF LNCAP-GAG	(416)	IEQVRAICLRAWGKIQDPGTAFF-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
GAG106-135	(31)	-----
GAG186-215	(31)	-----
GAG46-75	(31)	-----
PDG-G1	(17)	-----
PGD-G2	(17)	-----
PGD-G3	(1)	-----
CONSENSUS	(421)	-----
GI_4185938_EMB_CAA76878.1_	481	540
GI_4185942_EMB_CAA76881.1_	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMYKAMLMAQAITGVVL
GI_4185946_EMB_CAA76884.1_	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMHKAMLMAQAITGVVL
GI_5931704_EMB_CAB56602.1_	(254)	-----
GAG OF AB047240	(475)	VELMAYENANPECQSAIKPLKGKVPAGDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
TRANSLATION OF ORF99	(480)	VELMAYENANPECQSAIKPLKGKVPAGDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
TRANSLATION OF G226TOP-LINK	(31)	-----
TRANSLATION OF G591TOP-LINK	(1)	-----
TRANSLATION OF LNCAP-GAG	(475)	VELMAYENANPECQSAIKPLKGKVPAGDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
GAG106-135	(31)	-----
GAG186-215	(31)	-----
GAG46-75	(31)	-----
PDG-G1	(17)	-----
PGD-G2	(17)	-----
PGD-G3	(1)	-----
CONSENSUS	(481)	-----
GI_4185938_EMB_CAA76878.1_	541	600
GI_4185942_EMB_CAA76881.1_	(536)	GGQVRTFGRKCYNCQIIGHLKNCVPVLNKQNITIQTATTG-REPPDLCPRCKKGKHWASQ
GI_4185946_EMB_CAA76884.1_	(536)	GGQVRTFGRKCYNCQIIGHLKNCVPVLNKQNITIQTATTG-REPPDLCPRCKKGKHWASQ
GI_5931704_EMB_CAB56602.1_	(254)	-----
GAG OF AB047240	(535)	GGQVRTFGKKCYNCQIIGHLRSCPVLNKQNIIINQAITAKNKKPSGLCPKCGKGKHWANQ
TRANSLATION OF ORF99	(540)	GGQVRTFGKKCYNCQIIGHLRSCPVLNKQNIIINQAITAKNKKPSGLCPKCGKGKHWANQ
TRANSLATION OF G226TOP-LINK	(31)	-----
TRANSLATION OF G591TOP-LINK	(1)	-----
TRANSLATION OF LNCAP-GAG	(535)	GGQVRTFGKKCYNCQIIGHLRSCPVLNKQNIIINQAITAKNKKPSGLCPKCGKGKHWANQ
GAG106-135	(31)	-----
GAG186-215	(31)	-----
GAG46-75	(31)	-----
PDG-G1	(17)	-----
PGD-G2	(17)	-----
PGD-G3	(1)	-----
CONSENSUS	(541)	-----

FIGURE 7 CONTD...

GI_4185938_EMB_CAA76878.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ	601
GI_4185942_EMB_CAA76881.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ	
GI_4185946_EMB_CAA76884.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(595)	CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFFPVQLFVFPQGFQGQQPQLKIPPLQGVSQLQQ	
TRANSLATION OF ORF99	(600)	CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFFPVQLFVFPQGFQGQQPQLKIPPLQGVSQLQQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(5)	CRSKFDKNGQPLSGNEQRGQPQAPQQ-	
TRANSLATION OF LNCAP-GAG	(595)	CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFFPVQLFVFPQGFQGQQPQLKIPPLQGVSQLQQ	660
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PGD-G2	(17)	-----	
PGD-G3	(1)	CRSKFDKNGQPLSGNE-	
CONSENSUS	(601)	C SKFDK GQPLSGN	

GI_4185938_EMB_CAA76878.1_	(654)	YNNCPPPQAAVQQ	661
GI_4185942_EMB_CAA76881.1_	(654)	YNNCPPPQAAVQQ	
GI_4185946_EMB_CAA76884.1_	(654)	YNNCPPPQAAVQQ	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(655)	SNSCPAPQQAAPQ	
TRANSLATION OF ORF99	(660)	SNSCPAPQQAAPQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(31)	-----	
TRANSLATION OF LNCAP-GAG	(655)	SNSCPAPQQAAPQ	673
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PGD-G2	(17)	-----	
PGD-G3	(17)	-----	
CONSENSUS	(661)		

FIGURE 8

GI_4185939_EMB_CAA76879.1_	(1)	MLTDLRAVN--AVIQPMGPLQGPLSPAMIPKDWPILLIIDLKDCFFTIPILAECQDCEKFA	1
GI_4185943_EMB_CAA76882.1_	(1)	MLTDLRAVNNAVIQPMGPLQGPLPSLAMIPKDWPILLIIDLKDCFFTIPILAECQDCEKFA	
GI_4185947_EMB_CAA76885.1_	(1)	MLTDLRAVN--AVIQPMGPLQGPLSPAMIPKDWPILLIIDLKDCFFTIPILAECQDCEKFA	
GI_5931705_EMB_CAB56603.1_	(1)	-----MIPKDWPILLIIDLKDCFFTIPILAECQDCEKFA	
ENV OF AB047240	(1)	-----	
TRANSLATION OF P386TOP-LINK	(1)	-----	
TRANSLATION OF POL349-LINK	(1)	-----	
LNCAP-GENOMEA-POLORF	(1)	-----	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	
TRANSLATION OF ORF111-10	(1)	-----	
PGD-P1	(1)	-----	
PGD-P2	(1)	-----	
PGDP3	(1)	-----	
CONSENSUS	(1)	-----	
GI_4185939_EMB_CAA76879.1_	(58)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	61
GI_4185943_EMB_CAA76882.1_	(61)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHYDDILC	
GI_4185947_EMB_CAA76885.1_	(58)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	
GI_5931705_EMB_CAB56603.1_	(32)	FTIPAINNKEPATRFQWKVLPGMLNSPTLCQTFVGRALQPVRDKFSDCYIIHYFDDILC	
ENV OF AB047240	(1)	-----	
TRANSLATION OF P386TOP-LINK	(1)	-----	
TRANSLATION OF POL349-LINK	(1)	-----	
LNCAP-GENOMEA-POLORF	(1)	-----	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	
TRANSLATION OF ORF111-10	(1)	-----	
PGD-P1	(1)	-----	
PGD-P2	(1)	-----	
PGDP3	(1)	-----	
CONSENSUS	(61)		
GI_4185939_EMB_CAA76879.1_	(58)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	120
GI_4185943_EMB_CAA76882.1_	(61)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHYDDILC	
GI_4185947_EMB_CAA76885.1_	(58)	FTIPAINNKEPATRFQWKVLPGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	
GI_5931705_EMB_CAB56603.1_	(32)	FTIPAINNKEPATRFQWKVLPGMLNSPTLCQTFVGRALQPVRDKFSDCYIIHYFDDILC	
ENV OF AB047240	(1)	-----	
TRANSLATION OF P386TOP-LINK	(1)	-----	
TRANSLATION OF POL349-LINK	(1)	-----	
LNCAP-GENOMEA-POLORF	(1)	-----	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	
TRANSLATION OF ORF111-10	(1)	-----	
PGD-P1	(1)	-----	
PGD-P2	(1)	-----	
PGDP3	(1)	-----	
CONSENSUS	(61)		

FIGURE 8 cont'd.

GI_4185939_EMB_CAA76879_1	121	(118) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKD	180
GI_4185943_EMB_CAA76882_1	(121)	AAEMKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKD	
GI_4185947_EMB_CAA76885_1	(118)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKD	
GI_5931705_EMB_CAB56603_1	(92)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKD	
ENV OF AB047240	(1)	(1)	
TRANSLATION OF P386TOP-LINK	(1)	(1)	
TRANSLATION OF POL349-LINK	(1)	(1)	
LNCAP-GENOMEA-POLORF	(1)	(1)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	(1)	
TRANSLATION OF ORF111-10	(1)	(1)	
PGD-P1	(1)	(1)	-IENRKIKPQKIEIRKD-
PGD-P2	(1)	(1)	
PGDP3	(1)	(1)	
CONSENSUS	(121)		
GI_4185939_EMB_CAA76879_1	181		240
GI_4185943_EMB_CAA76882_1	(178)	LKTLNDFQKLIGDINWIRPTLGIPTYAMSNLFSLRGSIDLNSKRMLTPEATKEIKLVEE	
GI_4185947_EMB_CAA76885_1	(181)	LKTLNDFQKLIGDINWIRPTLGIPTYAMSNLFSLRGSIDLNSKRMLTPEATKEIKLVEE	
GI_5931705_EMB_CAB56603_1	(178)	LKTLNDFQKLIGDINWIRPTLGIPTYAMSNLFSLRGSIDLNSKRMLTPEATKEIKLVEE	
ENV OF AB047240	(152)	LKTLNDFQKLIGDINWIRPTLGIPTYAMSNLFSLRGSIDLNSKRMLTPEATKEIKLVEE	
TRANSLATION OF P386TOP-LINK	(1)	(1)	
TRANSLATION OF POL349-LINK	(1)	(1)	
LNCAP-GENOMEA-POLORF	(1)	(1)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	(1)	
TRANSLATION OF ORF111-10	(1)	(1)	
PGD-P1	(17)	(1)	
PGD-P2	(1)	(1)	
PGDP3	(1)	(1)	
CONSENSUS	(181)		
GI_4185939_EMB_CAA76879_1	241		300
GI_4185943_EMB_CAA76882_1	(238)	KIQSAQINRIDPLAPLQLILIFATAHSPTGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	
GI_4185947_EMB_CAA76885_1	(241)	KIQSAQINRIDPLAPLQLILIFATAHSPTGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	
GI_5931705_EMB_CAB56603_1	(238)	KIQSAQINRIDPLAPLQLILIFATAHSPTGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	
ENV OF AB047240	(212)	KIQSAQINRIDPLAPLQLILIFATAHSPTGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	
TRANSLATION OF P386TOP-LINK	(1)	(1)	
TRANSLATION OF POL349-LINK	(1)	(1)	
LNCAP-GENOMEA-POLORF	(1)	(1)	-DHLAPLQLILIFATAHSLTIIQNTDLVWSFLPHSTVKTFTLYLDQMAT
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	(1)	-DHLAPLQLILIFATAHSLTIIQNTDLVWSFLPHSTVKTFTLYLDQMAT
TRANSLATION OF ORF111-10	(1)	(1)	-YKKAGSDHPLQLILIFATAHSLTIIQNTDLVWSFLPHSTVKTFTLYLDQMAT
PGD-P1	(17)	(1)	
PGD-P2	(1)	(1)	
PGDP3	(1)	(1)	
CONSENSUS	(241)	D LAPLQLLIFATAHS TGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	
GI_4185939_EMB_CAA76879_1	301		360
GI_4185943_EMB_CAA76882_1	(298)	LIGQTRLRIITLKGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFGIIDNHYPKTKIF	
GI_4185947_EMB_CAA76885_1	(301)	LIGQTRLRIITLKGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFGIIDNHYPKTKIF	
GI_5931705_EMB_CAB56603_1	(298)	LIGQTRLRIITLKGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFGIIDNHYPKTKIF	
ENV OF AB047240	(272)	LIGQTRLRIITLKGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFGIIDNHYPKTKIF	
TRANSLATION OF P386TOP-LINK	(4)	LIGQGRRLIITLKGNDPDKITVPPFKQQVRAFISSGAWQIGLANFGIIDNHYPKTKIF	
TRANSLATION OF POL349-LINK	(1)	(1)	-NHYPKTKIF
LNCAP-GENOMEA-POLORF	(1)	(1)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(51)	LIGOGRRLIITLKGNDPDKITVPPFKQQVRAFISSGAWQIGLANFGIIDNHYPKTKIF	
TRANSLATION OF ORF111-10	(51)	LIGOGRRLIITLKGNDPDKITVPPFKQQVRAFISSGAWQIGLANFGIIDNHYPKTKIF	
PGD-P1	(57)	LIGOGRRLIITLKGNDPDKITVPPFKQQVRAFISSGAWQIGLANFGIIDNHYPKTKIF	
PGD-P2	(17)	(1)	
PGDP3	(1)	(1)	
CONSENSUS	(301)	LIGQ RLRII LCNDPDKI VP K QVRQAFI SGAW IGLANFLGIIDNHYPKTKIF	
GI_4185939_EMB_CAA76879_1	361		420
GI_4185943_EMB_CAA76882_1	(358)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
GI_4185947_EMB_CAA76885_1	(361)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
GI_5931705_EMB_CAB56603_1	(358)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
ENV OF AB047240	(332)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
TRANSLATION OF P386TOP-LINK	(64)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
TRANSLATION OF POL349-LINK	(1)	(1)	-GSSNGKAAYTGPKERVKTPYQSAQRAELVAV
LNCAP-GENOMEA-POLORF	(10)	(1)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(111)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
TRANSLATION OF ORF111-10	(111)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	
PGD-P1	(17)	(1)	-KAAYTGPKERVKTPC-
PGD-P2	(1)	(1)	
PGDP3	(1)	(1)	
CONSENSUS	(361)	QFLKLTIWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVKTPYQSAQRAELVAV	

FIGURE 8 CONTD...

<p>GI_4185939_EMB_CAA76879.1_</p> <p>GI_4185943_EMB_CAA76882.1_</p> <p>GI_4185947_EMB_CAA76885.1_</p> <p>GI_5931705_EMB_CAB56603.1_</p> <p>ENV OF AB047240</p> <p>TRANSLATION OF P386TOP-LINK</p> <p>TRANSLATION OF POL349-LINK</p> <p>LNCAP-GENOMEA-POLORF</p> <p>TRANSLATION OF LNCAP-POL-GENA-GOODA</p> <p>TRANSLATION OF ORF111-10</p> <p>PGD-P1</p> <p>PGD-P2</p> <p>PGDP3</p> <p>CONSENSUS</p>	421 (418) ITVLQDFDOPINISDSAYVQATRDVETALIKYSMDDQLNQLFNLLQOTVRKRNFPPFYI (421) ITVLQDFDOPINISDSAYVQATRDVETALIKYSMDDQLNQLFNLLQOTVRKRNFPPFYI (418) ITVLQDFDQPINISDSAYVQATRDVETALIKYSMDDQLNQLFNLLQOTVRKRNFPPFYI (392) ITVLQDFDOPINISDSAYVQATRDVETALIKYSMDDQLNQLFNLLQOTVRKRNFPPFYI (124) ITVLQDFDQPINISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQOTVRKRNFPPFYI (31) ----- (28) ----- (171) ITVLQDFDQPINISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQOTVRKRNFPPFYI (171) ITVLQDFDQPINISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQOTVRKRNFPPFYI (177) ITVLQDFDQPINISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQOTVRKRNFPPFYI (17) ----- (17) ----- (1) ----- (421) ITVLQDFDQPINISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQOTVRKRNFPPFYI	480
<p>GI_4185939_EMB_CAA76879.1_</p> <p>GI_4185943_EMB_CAA76882.1_</p> <p>GI_4185947_EMB_CAA76885.1_</p> <p>GI_5931705_EMB_CAB56603.1_</p> <p>ENV OF AB047240</p> <p>TRANSLATION OF P386TOP-LINK</p> <p>TRANSLATION OF POL349-LINK</p> <p>LNCAP-GENOMEA-POLORF</p> <p>TRANSLATION OF LNCAP-POL-GENA-GOODA</p> <p>TRANSLATION OF ORF111-10</p> <p>PGD-P1</p> <p>PGD-P2</p> <p>PGDP3</p> <p>CONSENSUS</p>	481 (478) THIRAHNTLPGPLTKANEQADLLVSSALIKAQELHALTHVNAGLKNKFDVTWKQAKDIV (481) THIRAHNTLPGPLTKANEQADLLVSSALIKAQELHALTHVNAGLKNKFDVTWKQAKDIV (478) THIRAHNTLPGPLTKANEQADLLVSSALIKAQELHALAHVNAGLKNKFDVTWKQAKDIV (452) THIRAHNTLPGPLTKANEQADLLVSSAFIKAQELHALTHVNAGLKNKFDVTWKQAKDIV (184) THIRAHNTLPGPLTKANEQADLLVSSAFIKAQELLAITHVNAGLKNKFDVTWKQAKDIV (31) ----- (28) ----- (231) THIRAHNTLPGPLTKANEQADLLVSSAFIKAQELLAITHVNAGLKNKFDVTWKQAKDIV (231) THIRAHNTLPGPLTKANEQADLLVSSAFIKAQELLAITHVNAGLKNKFDVTWKQAKDIV (237) THIRAHNTLPGPLTKANEQADLLVSSAFIKAQELLAITHVNAGLKNKFDVTWKQAKDIV (17) ----- (17) ----- (1) ----- (481) THIRAHNTLPGPLTKANEQADLLVSSA IKAQEL ALTHVNAGLKNKFDVTWKQAKDIV	540
<p>GI_4185939_EMB_CAA76879.1_</p> <p>GI_4185943_EMB_CAA76882.1_</p> <p>GI_4185947_EMB_CAA76885.1_</p> <p>GI_5931705_EMB_CAB56603.1_</p> <p>ENV OF AB047240</p> <p>TRANSLATION OF P386TOP-LINK</p> <p>TRANSLATION OF POL349-LINK</p> <p>LNCAP-GENOMEA-POLORF</p> <p>TRANSLATION OF LNCAP-POL-GENA-GOODA</p> <p>TRANSLATION OF ORF111-10</p> <p>PGD-P1</p> <p>PGD-P2</p> <p>PGDP3</p> <p>CONSENSUS</p>	541 (538) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC (541) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC (538) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC (512) QHCTOCVLHLPLTQEAGVNPEVCVLMHYGKWMGSHMLHLGRRLSYVHVTVDTYSHFIWATC (244) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC (31) ----- (28) ----- (291) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC (291) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC (297) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC (17) ----- (17) ----- (1) ----- (541) QHCTOCVLHLPLTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC	600
<p>GI_4185939_EMB_CAA76879.1_</p> <p>GI_4185943_EMB_CAA76882.1_</p> <p>GI_4185947_EMB_CAA76885.1_</p> <p>GI_5931705_EMB_CAB56603.1_</p> <p>ENV OF AB047240</p> <p>TRANSLATION OF P386TOP-LINK</p> <p>TRANSLATION OF POL349-LINK</p> <p>LNCAP-GENOMEA-POLORF</p> <p>TRANSLATION OF LNCAP-POL-GENA-GOODA</p> <p>TRANSLATION OF ORF111-10</p> <p>PGD-P1</p> <p>PGD-P2</p> <p>PGDP3</p> <p>CONSENSUS</p>	601 (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (572) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (304) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (31) ----- (28) ----- (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (357) QTGESTSHAKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG (17) ----- (17) ----- (1) ----- (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG	660
<p>GI_4185939_EMB_CAA76879.1_</p> <p>GI_4185943_EMB_CAA76882.1_</p> <p>GI_4185947_EMB_CAA76885.1_</p> <p>GI_5931705_EMB_CAB56603.1_</p> <p>ENV OF AB047240</p> <p>TRANSLATION OF P386TOP-LINK</p> <p>TRANSLATION OF POL349-LINK</p> <p>LNCAP-GENOMEA-POLORF</p> <p>TRANSLATION OF LNCAP-POL-GENA-GOODA</p> <p>TRANSLATION OF ORF111-10</p> <p>PGD-P1</p> <p>PGD-P2</p> <p>PGDP3</p> <p>CONSENSUS</p>	661 (658) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (661) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (658) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (632) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (364) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (31) ----- (28) ----- (411) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (411) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (417) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT (17) ----- (17) ----- (1) ----- (661) QAIVERTNRTLTKTOLVKQKEGGDSKECTTPQMQLNIALYTLNFLNLYRNQTTTSAKQHLT	720

FIGURE 8 contd...

721 780

GI_4185939_EMB_CAA76879.1_	(718) GKKNSPHEGKLIWWKDKSNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_4185943_EMB_CAA76882.1_	(721) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_4185947_EMB_CAA76885.1_	(718) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_5931705_EMB_CAB56603.1_	(691) GKKNSPHEGKLI-----
ENV OF AB047240	(424) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
TRANSLATION OF P386TOP-LINK	(31) -----
TRANSLATION OF POL349-LINK	(28) -----
LNCAP-GENOMEA-POLORF	(471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
TRANSLATION OF LNCAP-POL-GENA-GOODA	(471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
TRANSLATION OF ORF111-10	(477) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
PGD-P1	(17) -----
PGD-P2	(17) -----
PGDP3	(4) GKKNSPHEGKLI-----
CONSENSUS	(721) GKK SPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI

781 840

GI_4185939_EMB_CAA76879.1_	(778) RDAKKSTSAAETETS-----
GI_4185943_EMB_CAA76882.1_	(781) GDAKKSTSAAETETP-----
GI_4185947_EMB_CAA76885.1_	(778) RDAKKSTSAAETETS-----
GI_5931705_EMB_CAB56603.1_	(703) -----
ENV OF AB047240	(484) GDAKKRASTEMVTPVTMDNPPIEVVVNDSVVVPGPTEDRCPAKPEEEGMMINISIVYRYP
TRANSLATION OF P386TOP-LINK	(31) -----
TRANSLATION OF POL349-LINK	(28) -----
LNCAP-GENOMEA-POLORF	(531) GDAKKRASTEMVTPVTMDNPPIEVVVNDSVVVPGPTEDRCPAKPEEEGMMINISIVYRYP
TRANSLATION OF LNCAP-POL-GENA-GOODA	(531) GDAKKRASTEMVTPVTMDNPPIEVVVNDSVVVPGPTEDRCPAKPEEEGMMINISIVYRYP
TRANSLATION OF ORF111-10	(537) GDAKKRASTEMVTPVTMDNPPIEVVVNDSVVVPGPTEDRCPAKPEEEGMMINISIVYRYP
PGD-P1	(17) -----
PGD-P2	(17) -----
PGDP3	(17) -----
CONSENSUS	(781) DAKK S E T

841 900

GI_4185939_EMB_CAA76879.1_	(792) -----
GI_4185943_EMB_CAA76882.1_	(795) -----
GI_4185947_EMB_CAA76885.1_	(792) -----
GI_5931705_EMB_CAB56603.1_	(703) -----
ENV OF AB047240	(544) PICLGRAPGCLMPAVQNWLVVEPVTSPNSRFTYHMGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF P386TOP-LINK	(31) -----
TRANSLATION OF POL349-LINK	(28) -----
LNCAP-GENOMEA-POLORF	(591) PICLGRAPGCLMPAVQNWLVVEPVTSPNSRFTYHMGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF LNCAP-POL-GENA-GOODA	(591) PICLGRAPGCLMPAVQNWLVVEPVTSPNSRFTYHMGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF ORF111-10	(597) PICLGRAPGCLMPAVQNWLVVEPVTSPNSRFTYHMGMSLRPRVNYLQDFSYQRSLKFR
PGD-P1	(17) -----
PGD-P2	(17) -----
PGDP3	(17) -----
CONSENSUS	(841) -----

901 960

GI_4185939_EMB_CAA76879.1_	(792) -----
GI_4185943_EMB_CAA76882.1_	(795) -----
GI_4185947_EMB_CAA76885.1_	(792) -----
GI_5931705_EMB_CAB56603.1_	(703) -----
ENV OF AB047240	(604) PKGKPCPKIEPKESKNTEVLVWEECVANSILQNEFGTIDWAPRGQFYHNCSGQTQS
TRANSLATION OF P386TOP-LINK	(31) -----
TRANSLATION OF POL349-LINK	(28) -----
LNCAP-GENOMEA-POLORF	(651) PKGKPCPKIEPKESKNTEVLVWEECVANSILQNEFGTIDWAPRGQFYHNCSGQTQS
TRANSLATION OF LNCAP-POL-GENA-GOODA	(651) PKGKPCPKIEPKESKNTEVLVWEECVANSILQNEFGTIDWAPRGQFYHNCSGQTQS
TRANSLATION OF ORF111-10	(657) PKGKPCPKIEPKESKNTEVLVWEECVANSILQNEFGTIDWAPRGQFYHNCSGQTQS
PGD-P1	(17) -----
PGD-P2	(17) -----
PGDP3	(17) -----
CONSENSUS	(901) TI

961 1020

GI_4185939_EMB_CAA76879.1_	(816) QEGRAANLTTKIADAVSYKISREHKGDTPREACSDDCINGGKSPYCRSSCS-----
GI_4185943_EMB_CAA76882.1_	(619) QESRAADLTTKIADAVSYKISREHKGDTPREACSDDCINGGKSPYCRSSCS-----
GI_4185947_EMB_CAA76885.1_	(816) QEGRAANLTTKIADAVSYKISREHKGDTPREACSDDCINGGKSPYCRSSCS-----
GI_5931705_EMB_CAB56603.1_	(703) -----
ENV OF AB047240	(664) CPSAQVSPVVDSELTESLDKHKHKLQLSFYPWEGKGSTPRPEIISPVGPEHPELWR
TRANSLATION OF P386TOP-LINK	(31) -----
TRANSLATION OF POL349-LINK	(28) -----
LNCAP-GENOMEA-POLORF	(711) CPSAQVSPVVDSELTESLDKHKHKLQLSFYPWEGKGSTPRPEIISPVGPEHPELWR
TRANSLATION OF LNCAP-POL-GENA-GOODA	(711) CPSAQVSPVVDSELTESLDKHKHKLQLSFYPWEGKGSTPRPEIISPVGPEHPELWR
TRANSLATION OF ORF111-10	(717) CPSAQVSPVVDSELTESLDKHKHKLQLSFYPWEGKGSTPRPEIISPVGPEHPELWR
PGD-P1	(17) -----
PGD-P2	(17) -----
PGDP3	(17) -----
CONSENSUS	(961) A D K P EWG I SP S

FIGURE 8 CONTD...

	1021	1035
GI_4185939_EMB_CAA76879.1_	(873)	-----
GI_4185943_EMB_CAA76882.1_	(876)	-----
GI_4185947_EMB_CAA76885.1_	(873)	-----
GI_5931705_EMB_CAB56603.1_	(703)	-----
ENV OF AB047240	(724)	LWPDTTLEFGGLEIKL
TRANSLATION OF P386TOP-LINK	(31)	-----
TRANSLATION OF POL349-LINK	(28)	-----
LNCAP-GENOMEA-POLORF	(764)	-----
TRANSLATION OF LNCAP-POL-GENA-GOODF	(771)	LWPDTTLEFGGLEIKL
TRANSLATION OF ORF111-10	(777)	LWPDTTLEFGGLEIKL
PGD-P1	(17)	-----
PGD-P2	(17)	-----
PGD-P3	(17)	-----
CONSENSUS	(1021)	

FIGURE 9

	1	60
GI_4185940_EMB_CAA76880.1_	(1)	-----
GI_4185944_EMB_CAA76883.1_	(1)	-----
GI_4185948_EMB_CAA76886.1_	(1)	-----
GI_5931706_EMB_CAB56604.1_	(1)	-----
ENV OF AB047240	(1)	MATLIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKT
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(1)	
	61	120
GI_4185940_EMB_CAA76880.1_	(1)	-----
GI_4185944_EMB_CAA76883.1_	(1)	-----
GI_4185948_EMB_CAA76886.1_	(1)	-----
GI_5931706_EMB_CAB56604.1_	(1)	-----
ENV OF AB047240	(61)	KIFQFLKLTTWILPKITRREPLENALTVDGSSNGKAAYTGPKERVIKTPYQSAQRUEL
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(61)	
	121	180
GI_4185940_EMB_CAA76880.1_	(1)	-----
GI_4185944_EMB_CAA76883.1_	(1)	-----
GI_4185948_EMB_CAA76886.1_	(1)	-----
GI_5931706_EMB_CAB56604.1_	(1)	-----
ENV OF AB047240	(121)	VAVITVLQDFDQPINIISDSAYVQATRDVETALIKYSTDDHNLNQLFNLLQQTVRKRNFP
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(121)	

FIGURE 9 CONTD...

GI_4185940_EMB_CAA76880.1	181	(1) -----	240
GI_4185944_EMB_CAA76883.1	(1) -----		
GI_4185948_EMB_CAA76886.1	(1) -----		
GI_5931706_EMB_CAB56604.1	(1) -----		
ENV OF AB047240	(181) FYIITHIRAHNTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAK		
TRANSLATION OF E207TOP-LINK	(1) -----		
TRANSLATION OF ENV287-LINK	(1) -----		
TRANSLATION OF T20..22A-23	(1) -----		
PGD-E1	(1) -----		
PGD-E2	(1) -----		
PGD-E3	(1) -----		
CONSENSUS	(181)		
GI_4185940_EMB_CAA76880.1	241	(1) -----	300
GI_4185944_EMB_CAA76883.1	(1) -----		
GI_4185948_EMB_CAA76886.1	(1) -----		
GI_5931706_EMB_CAB56604.1	(1) -----		
ENV OF AB047240	(241) DIVQHCTQCQLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIW		
TRANSLATION OF E207TOP-LINK	(1) -----		
TRANSLATION OF ENV287-LINK	(1) -----		
TRANSLATION OF T20..22A-23	(1) -----		
PGD-E1	(1) -----		
PGD-E2	(1) -----		
PGD-E3	(1) -----		
CONSENSUS	(241)		
GI_4185940_EMB_CAA76880.1	301	(1) -----	360
GI_4185944_EMB_CAA76883.1	(1) -----		
GI_4185948_EMB_CAA76886.1	(1) -----		
GI_5931706_EMB_CAB56604.1	(1) -----		
ENV OF AB047240	(301) ATCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYN		
TRANSLATION OF E207TOP-LINK	(1) -----		
TRANSLATION OF ENV287-LINK	(1) -----		
TRANSLATION OF T20..22A-23	(1) -----		
PGD-E1	(1) -----		
PGD-E2	(1) -----		
PGD-E3	(1) -----		
CONSENSUS	(301)		
GI_4185940_EMB_CAA76880.1	361	(1) -----	420
GI_4185944_EMB_CAA76883.1	(1) -----		
GI_4185948_EMB_CAA76886.1	(1) -----		
GI_5931706_EMB_CAB56604.1	(1) -----		
ENV OF AB047240	(361) SQGQAIVERTNRLKTQLVKQKEGGDSKECTTPQMLNLALYTLNFLNIYRNQTTSAKQ		
TRANSLATION OF E207TOP-LINK	(1) -----		
TRANSLATION OF ENV287-LINK	(1) -----		
TRANSLATION OF T20..22A-23	(1) -----		
PGD-E1	(1) -----		
PGD-E2	(1) -----		
PGD-E3	(1) -----		
CONSENSUS	(361)		
GI_4185940_EMB_CAA76880.1	421	(35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVQTPESMILLAALMIVSMVVSLPMPAGAAAA	480
GI_4185944_EMB_CAA76883.1	(35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVQTPESMILLAALMIVSMVVSLPMPAGAAAA		
GI_4185948_EMB_CAA76886.1	(35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVQTPESMILLAALMIVSMVVSLPMPAGAAAA		
GI_5931706_EMB_CAB56604.1	(1) -----		
ENV OF AB047240	(421) HLTKKHSPEGKLIWWKDNKNKTWEIGKVITWGRRGFACVSPGENOLPVWIPTRHLKFYN		
TRANSLATION OF E207TOP-LINK	(1) -----		
TRANSLATION OF ENV287-LINK	(1) -----		
TRANSLATION OF T20..22A-23	(40) PSTKKAEPPTWAQLKKLTQLATKYLENTKVQTPESMILLAALMIVSMVVSLPMPAGAAAA		
PGD-E1	(1) -----		
PGD-E2	(1) -----		
PGD-E3	(1) -----		
CONSENSUS	(421)		

FIGURE 9 CONTD...

GI_4185940_EMB_CAA76880.1	(95)	NYTYWAYVPFPPII	RAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY	481	540
GI_4185944_EMB_CAA76883.1	(95)	NYTYWAYVPFPPII	RAVTWMDNPIEVYVNDSVWVPGPTDDHCPAKPEEEGMMINISIGY		
GI_4185948_EMB_CAA76886.1	(95)	NYTYWAYVPFPPII	RAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY		
GI_5931706_EMB_CAB56604.1	(1)	-----	WTPVTWMDNPIEVYVNDSVWVPGPTDDHCPAKPEEEGMMINISIGY		
ENV OF AB047240	(481)	EPIDAKKRASTER	WTPVTWMDNPIEVYVNDSVWVPGPTDDHCPAKPEEEGMMINISIVY		
TRANSLATION OF E207TOP-LINK	(1)	-----			
TRANSLATION OF ENV287-LINK	(1)	-----			
TRANSLATION OF T20.22A-23	(100)	NYTYWAYVPFPPII	RAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY		
PGD-E1	(1)	-----			
PGD-E2	(1)	-----			
PGD-E3	(1)	-----			
CONSENSUS	(481)	LI	VTWMDNP EVYVNDSVWVPGP DD CPAKPEEEGMMINISI Y		
GI_4185940_EMB_CAA76880.1	(154)	HYPPICLGRAPGC	MPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNLYQDFSYQRSL	541	600
GI_4185944_EMB_CAA76883.1	(154)	RYPPICLGRAPGC	MPAVQNWLVEVPTVSPISRFTYHMVSGMSLRPRVNLYQDFSYQRSL		
GI_4185948_EMB_CAA76886.1	(154)	HYPPICLGRAPGC	MPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNLYQDFSYQRSL		
GI_5931706_EMB_CAB56604.1	(48)	HYPPICLGRAPGC	MPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNCLQDFSYQRSL		
ENV OF AB047240	(541)	RYPPICLGRAPGC	MPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNLYQDFSYQRSL		
TRANSLATION OF E207TOP-LINK	(1)	-----			
TRANSLATION OF ENV287-LINK	(1)	-----			
TRANSLATION OF T20.22A-23	(159)	HYPPICLGRAPGC	MPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNLYQDFSYQRSL		
PGD-E1	(1)	-----			
PGD-E2	(1)	-----			
PGD-E3	(1)	-----			
CONSENSUS	(541)	YPPICLGRAPGC	MPAVQNWLVEVPTVSP RFTYHMVSGMSLRPRVN LQDFSYQRSL		
GI_4185940_EMB_CAA76880.1	(214)	KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ	601	660	
GI_4185944_EMB_CAA76883.1	(214)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
GI_4185948_EMB_CAA76886.1	(214)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
GI_5931706_EMB_CAB56604.1	(108)	KFRPKGKTCPKBIPKGSKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
ENV OF AB047240	(601)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
TRANSLATION OF E207TOP-LINK	(8)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
TRANSLATION OF ENV287-LINK	(1)	-----			
TRANSLATION OF T20.22A-23	(219)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANSAILQNNEGFTIIDWAPRGQFYHNCSGQ			
PGD-E1	(1)	--RPGKPCPKBIPKESC			
PGD-E2	(1)	-----			
PGD-E3	(1)	-----			
CONSENSUS	(601)	KFRPKGKPCPKBIPKESKNTEVLVWEECVANS VILQNNEGFTIIDWAPRGQFYHNCSGQ			
GI_4185940_EMB_CAA76880.1	(274)	TOSCOQAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI	661	720	
GI_4185944_EMB_CAA76883.1	(274)	TQSCPSAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
GI_4185948_EMB_CAA76886.1	(274)	TQSCPSAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
GI_5931706_EMB_CAB56604.1	(168)	TQSCPSAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
ENV OF AB047240	(661)	TQSCPSAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
TRANSLATION OF E207TOP-LINK	(31)	-----			
TRANSLATION OF ENV287-LINK	(1)	--SDLTESLDKHHKKLQSFPWEWGEKGII			
TRANSLATION OF T20.22A-23	(279)	TQSCPSAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
PGD-E1	(17)	-----			
PGD-E2	(1)	-----			
PGD-E3	(1)	-----			
CONSENSUS	(661)	TQSC SAQVSPAVDSLTESLDKHHKKLQSFPWEWGEKGISTPRPKI			
GI_4185940_EMB_CAA76880.1	(334)	LWRLTVASHHIREWSGNQTLERDRKPFYTIIDLNSS	721	780	
GI_4185944_EMB_CAA76883.1	(334)	LWRLTVASHHIREWSGNQTLERDRKPFYTIIDLNSS			
GI_4185948_EMB_CAA76886.1	(334)	LWRLTVASHHIREWSGNQTLERDRKPFYTIIDLNSS			
GI_5931706_EMB_CAB56604.1	(228)	LWRLTVASHHIREWSGNQTLERTRKPFYTIIDLNSI			
ENV OF AB047240	(721)	LW-----RI-----W-----P-----			
TRANSLATION OF E207TOP-LINK	(31)	-----			
TRANSLATION OF ENV287-LINK	(29)	-----			
TRANSLATION OF T20.22A-23	(339)	LWRLTVASHHIREWSGNQTLERDRKPFYTIIDLNSS			
PGD-E1	(17)	-----			
PGD-E2	(1)	-----			
PGD-E3	(1)	-----			
CONSENSUS	(721)	LW RI LNS TVPLQSCVKP			

FIGURE 9 CONTD...

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	781 (394) DSQTITCENCRLLT CID STF N QH RILL V RAREGV W I P V S M D R P W E A S P V H I L T E V L K G (394) DSQTITCENCRLLT CID STF N QH RILL V RAREGV W I P V S M D R P W E T S P S I H T L T E V L K G (394) DSQTITCENCRLLT CID STF N QH RILL V RAREGV W I P V S M D R P W E A S P V H I L T E V L K G (288) ASQTITCENCRLFT CID STF N QH RILL V RAREGMW I P V S M D R P W E A S P S I H I L T E V L K G (727) ----- D T L E S C L E I K L ----- (31) ----- (29) ----- (399) DSQTITCENCRLLT CID STF N QH RILL V RAREGV W I P V S M D R P W E A S P V H I L T E V L K G (17) ----- PGD-E2 (17) ----- PGD-E3 (1) ----- CONSENSUS (781) DST W I L

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	840 (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNNSQSSI (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNNSQSSI (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNNSQSSI (348) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTRLWNNSQSSI (739) ----- (31) ----- (29) ----- (459) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNNSQSSI (17) ----- (17) ----- (1) ----- CONSENSUS (841)

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	900 (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFSITPQIYNSEHHWDMVRHH (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSESELHWDMDVRHH (408) DQKLASQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (739) ----- (31) ----- (29) ----- (519) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (17) ----- (17) ----- (1) ----- CONSENSUS (901)

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	960 (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFSITPQIYNSEHHWDMVRHH (514) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSESELHWDMDVRHH (408) DQKLASQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (739) ----- (31) ----- (29) ----- (519) DQKLANQINDLRQTVIWMGDRLLMSLEHRFQLQCDWNTSDFCITPQIYNSEHHWDMVRHH (17) ----- (17) ----- (1) ----- CONSENSUS (901)

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	961 (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (468) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (739) ----- (31) ----- (29) ----- (519) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (17) ----- (17) ----- (1) ----- CONSENSUS (961)

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	1020 (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (574) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (468) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (739) ----- (31) ----- (29) ----- (519) LQGREDNLTL DISKLKE Q I F E A S K A H L N L V P G T E A I A G V A D G L A N L N P V T W V K T I G S T T I (17) ----- (17) ----- (1) ----- CONSENSUS (961)

GI_4185940_EMB_CAA76880.1 GI_4185944_EMB_CAA76883.1 GI_4185948_EMB_CAA76886.1 GI_5931706_EMB_CAB56604.1 ENV OF AB047240 TRANSLATION OF E207TOP-LINK TRANSLATION OF ENV287-LINK TRANSLATION OF T20.22A-23 PGD-E1 PGD-E2 PGD-E3 CONSENSUS	1081 (634) INLILILVCLFCLLLVCRCTQQLRRSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV (634) INLILILVCLFCLLLVCRCTQQLRRSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV (634) INLILILVCLFCLLLVCRCTQQLRRSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV (528) INLILILVCLFCLLLVCRCTQQLRRSDSIENG----- (739) ----- (31) ----- (29) ----- (639) INLILILVCLFCLLLVCRCTQQLRRSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV (17) ----- (17) ----- (1) ----- RCTQQLRRSDHRERA----- CONSENSUS (1021) RCTQQLRRSD